SEQ ID NO:1   FIGURE 1

CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGA
AGTGACGGGGGGTGGGATTGAATGAAAAGTGCAAAACACAGGCTCGCAGCGCTGGA
GCCCGGGGCCGCGGAGCCGGGCCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGG
GGGCGCCCTGCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCG
CGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACTAGCCCCCAACTTT
GGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCCACGCGGCGCGCCGGGGCCGCGGA
CGGCAGCGGCCCCCGGGGATGCGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCT
GCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAGCT
GCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGG
ACAGCGACGCGGACAGCATCAGCCTCGAGCTGCGCAAGCCCGACGGCACCCTCGTC
TCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGG
GAGCTGGAGAAGGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCA
GCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCAGAAAAATCCCC
GGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTC
GCTGTCAACTTCAGCCAGGGGGCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCC
GAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAGCA
AGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGC
TGCCTCGCTGCAGGCAGGTGGGGGACCGCGGGAAGCCCTGCGTCTGCCACTATGGC
CTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCC
ACGCCCTACAAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTAC
GTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCCAGGCTAGGGTGG
GAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGG
GGGTGGCAACCCCCACCTGAGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTA
GAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATGGCA
GGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAG
GGAGAGAAGGGCTCCCCAGATCTACACCCCTCCCTCCTGCATCTCCCCTGGAGTGTT
CACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAAC
GTTTAGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCC
TTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCAGTCCCTTCCTACTCCCCAAC
AAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTG
TACTGGATTACAGCATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGG
AGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCCGGACCTGGAC
GTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAA
GGTTCTGGGGCAGGGAGGGAGCATGAAGTACGAGGAAAACTTGAATTCCAGATTTT
TAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGACT
AATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGA
AAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGGAACAAGAACTTCGAAAGCACCT

FIGURE 1 (continued)

ACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGA
AGGATGAGATAAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGT
AGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGGTGGAGATTGGA
ACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTT
GCTTGACCTCTCTGTGCCTCCACTCCCTTAGCTATAAAATGAGCTTACTT

SEQ ID NO:2   FIGURE 2

MRLPGVPLARPALLLLLPLLAPLLGTGAPAELRVRVRLPDGQVTEESLQADSDADSISLEL
RKPDGTLVSFTADFKKDVKVFRALILGELEKGQSQFQALCFVTQLQHNEIIPSEAMAKLR
QKNPRAVRQAEEVRGLEHLHMDVAVNFSQGALLSPHLHNVCAEAVDAIYTRQEDVRF
WLEQGVDSSVFEALPKASEQAELPRCRQVGDRGKPCVCHYGLSLAWYPCMLKYCHSR
DRPTPYKCGIRSCQKSYSFDFYVPQRQLCLWDEDPYPG*

SEQ ID NO:3   FIGURE 3

MRLPGVPLARPALLLLLPLLAPLLG TGAPA

FIGURE 4

Sequence Range: 1 to 2366

```
                  10        20        30        40        50        60        70        80        90
SEQ ID NO:1  CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGAAGTGACGGGGGGTGGGATTGAATGAAAAGTGCA
             GGCGCTCCACGCGCCAGAGAAATTCCGCCCAGGACCACCAAAGACAAAGGACTTCCTTCACTGCCCCCCACCCTAACTTACTTTTCACGT
                  100       110       120       130       140       150       160       170       180
             AAACACAGGCTCGCAGCGCTGGAGCCCGGGGCCGCGGAGCCGGGCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGGGGGCGCCCTGC
             TTTGTGTCCGAGCGTCGCGACCTCGGGCCCCGGCGCCTCGGCCCGGCCCCGTCGCGGCAGAGGCGGAGCCCCGGCGGCCCCCGCGGGACG
                  190       200       210       220       230       240       250       260       270
             TGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCGCGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACTAG
             ACTCGCGATGGGTGCACGCAGGCGCGGTGGAGCGCCCGCTGGGGCGCCGGTTCCGGGGGCGCGCCTCGCCGAGGGCCCGCGGGGCTTGATC

                  280       290       300       310       320       330       340       350       360
             CCCCCAACTTTGGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCCACGCGGCGCGCCGGGGCCGCGGACGGCAGCGGCCCCCGGGGATGCG
             GGGGGTTGAAACCCGCTTCAAACGGACGCGGAGAGGGGCGGGGGTGCGCCGCGCGCGGCCCCGGCGCCTGCCGTCGCCGGGGGCCCCTACGC
SEQ ID NO:2                                                                                        M  R>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  370       380       390       400       410       420       430       440       450
             CCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCTGCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAGCT
             GGAAGGGCCCCATGGGGACCGCGCGGGACGCGACGACGACGACGACGGCGACGAGCGCGCGGCGACGACCCTTGCCCACGCGGCCGGCTCGA
               L  P  G  V  P  L  A  R  P  A  L  L  L  L  L  P  L  L  A  P  L  L  G  T  G  A  P  A  E  L>
             _____ TRANSLATION OF OAFHUMAN [A]_____  _____>

                  460       470       480       490       500       510       520       530       540
             GCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGGACAGCGACGCGGACAGCATCAGCCTCGAGCTGCG
             CGCCCAGGCGCACGCCGACGGCCTGCCGGTCCACTGGCTCCTCTCGGACGTCCGCCTGTCGCTGCGCCTGTCGTAGTCGGAGCTCGACGC
               R  V  R  V  R  L  P  D  G  Q  V  T  E  E  S  L  Q  A  D  S  D  A  D  S  I  S  L  E  L  R>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  550       560       570       580       590       600       610       620       630
             CAAGCCCGACGGCACCCTCGTCTCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGGGAGCTGGAGAA
             GTTCGGGCTGCCGTGGGAGCAGAGGAAGTGGCGGCTGAAGTTCTTCCTACACTTCCAGAAGGCCCGGGACTAGGACCCCCTCGACCTCTT
               K  P  D  G  T  L  V  S  F  T  A  D  F  K  K  D  V  K  V  F  R  A  L  I  L  G  E  L  E  K>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  640       650       660       670       680       690       700       710       720
             GGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCAGCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGGCA
             CCCCGTCTCAGTCAAGGTCCGGGAGACGAAACAGTGGGTCGACGTCGTGTTACTCTAGTAGGGGTCACTCCGGTACCGGTTCGAGGCCGT
               G  Q  S  Q  F  Q  A  L  C  F  V  T  Q  L  Q  H  N  E  I  I  P  S  E  A  M  A  K  L  R  Q>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  730       740       750       760       770       780       790       800       810
             GAAAAATCCCCGGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGGGC
             CTTTTTAGGGGCCCGTCACGCCGTCCGCCTCCTCCAAGCCCCAGACCTCGTAGACGTGTACCTACAGCGACAGTTGAAGTCGGTCCCCCG
               K  N  P  R  A  V  R  Q  A  E  E  V  R  G  L  E  H  L  H  M  D  V  A  V  N  F  S  Q  G  A>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  820       830       840       850       860       870       880       890       900
             CCTGCTGAGCCCCCATCTCCACAACGTGTGTGCCGAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAGCA
             GGACGACTCGGGGGTAGAGGTGTTGCACACACGGCTCCGGCACCTACGGTAGATGTGGGCGGTCCTCCTACAGGCCAAGACCGACCTCGT
               L  L  S  P  H  L  H  N  V  C  A  E  A  V  D  A  I  Y  T  R  Q  E  D  V  R  F  W  L  E  Q>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  910       920       930       940       950       960       970       980       990
             AGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGCTGCCTCGCTGCAGGCAGGTGGGGGACCGCGGGAA
             TCCACACCTGTCAAGACACAAGCTCCGAGACGGGTTCCGGAGTCTCGTCCGCCTCGACGGAGCGACGTCCGTCCACCCCCTGGCGCCCTT
               G  V  D  S  S  V  F  E  A  L  P  K  A  S  E  Q  A  E  L  P  R  C  R  Q  V  G  D  R  G  K>
             _____ TRANSLATION OF OAFHUMAN [A]_____>

                  1000      1010      1020      1030      1040      1050      1060      1070      1080
             GCCCTGCGTCTGCCACTATGGCCTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCCACGCCCTACAA
             CGGGACGCAGACGGTGATACCGGACTCGGACCGGACCATGGGGACGTACGAGTTCATGACGGTGTCGGCGCTGGCCGGGTGCGGGATGTT
               P  C  V  C  H  Y  G  L  S  L  A  W  Y  P  C  M  L  K  Y  C  H  S  R  D  R  P  T  P  Y  K>
```

FIGURE 4 (continued)

```
        1090      1100      1110      1120      1130      1140      1150      1160      1170
GTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTACCC
CACACCGTAGGCGTCGACGGTCTTCTCGATGTCGAAGCTGAAGATGCACGGGGTCTCCGTCGACACAGAGACCCTACTCCTAGGGATGGG
   C   G   I   R   S   C   Q   K   S   Y   S   F   D   F   Y   V   P   Q   R   Q   L   C   L   W   D   E   D   P   Y   P>
_____TRANSLATION OF OAFHUMAN [A]_____>

        1180      1190      1200      1210      1220      1230      1240      1250      1260
AGGCTAGGGTGGGAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGGGGGTGGCAACCCCCACCTGAG
TCCGATCCCACCCTCGTTGGACCCGCCCACCGACGAGACCCGGGTGACGAGAAGTGGTCGGTGATCTCCCCCACCGTTGGGGGTGGACTC
   G   *

        1270      1280      1290      1300      1310      1320      1330      1340      1350
GCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTAGAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCATG
CGGAATAAAGGGAGGGAGGGGTGAGGGGACCGGGATCTCGGACCCGGGGAGACCGGGGTAGAGTGTACTGACACTTCCCCCACACCGTAC

        1360      1370      1380      1390      1400      1410      1420      1430      1440
GCAGGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAGGGAGAGAAGGGCTCCCCAGATCTACACCCC
CGTCCCCCAGAGTACTTCCGTGGGGGTAAGGGTGGGACACGGAAGGAACGCCCGTCTCTCCCTCTCTTCCCGAGGGGTCTAGATGTGGGG

        1450      1460      1470      1480      1490      1500      1510      1520      1530
TCCCTCCTGCATCTCCCCTGGAGTGTTCACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAACGTTTAG
AGGGAGGACGTAGAGGGGACCTCACAAGTGAACGTTCGACGGTTTTGTACTACCGGAGACCAACAAGACAACTTGAGGAACTTGCAAATC

        1540      1550      1560      1570      1580      1590      1600      1610      1620
ACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGACACAACTCCCTTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCAGT
TGGGATTTTCCTCAGATATGGACCTGTGGGTGGAGGGGTCTGTGTTGAGGGAAGGGGTACGTGTGTAGACCTTCCTCGACCGGGGAGTCA

        1630      1640      1650      1660      1670      1680      1690      1700      1710
CCCTTCCTACTCCCCAACAAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTGTACTGGATTACAGCAT
GGGAAGGATGAGGGGTTGTTCCCCGAGTGATAGGGGTTTCTTCCTCGACAACCCCTGGGTGCTGCGTCGGGGACATGACCTAATGTCGTA

        1720      1730      1740      1750      1760      1770      1780      1790      1800
ATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGGAGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCCGG
TAAGAGTAGAGACCGGGGCTCCGACGGACACCCCGCTCACCTCTGGAGGGTAGTGACTCTGTCTAGTGTCTGGTGCTCACGGAAAGGGCC

        1810      1820      1830      1840      1850      1860      1870      1880      1890
ACCTGGACGTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAAGGTTCTGGGGCAGGGAGGGAGCATG
TGGACCTGCAACGGAGGTTTTGTCCGTGGTCGAGAAAGGGAGAGATCTGTCTTTATAAAAACATTCCAAGACCCCGTCCCTCCCTCGTAC

        1900      1910      1920      1930      1940      1950      1960      1970      1980
AAGTACGAGGAAAACTTGAATTCCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGACTA
TTCATGCTCCTTTTGAACTTAAGGTCTAAAAATTACGTTTCATAAATAGTAAAGATGGTCTTTATTTGCAAAATTCAAAAATGAACTGAT

        1990      2000      2010      2020      2030      2040      2050      2060      2070
ATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCCTAGCAGTGGCCTATCTTGG
TACTCTGGGTCTCAAACCTCTTTTGAAAACCGGTTACGACGGTGGACTACAGTCTTTCACAGGGGTGTGGGATCGTCACCGGATAGAACC

        2080      2090      2100      2110      2120      2130      2140      2150      2160
AACAAGAACTTCGAAAGCACCTACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGAAGGATGAGATAA
TTGTTCTTGAAGCTTTCGTGGATGACACACGAGTCGGTAAACTCCTTCCTTCCTCCTCTTCCTTCTACAATGATCCCTTCCTACTCTATT

        2170      2180      2190      2200      2210      2220      2230      2240      2250
AACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGGTG
TTGAAGACGTGGGTTCTGTTACTCTGTCTGTATTGACGTTGGCATCATTCGGTCAGTCTTTATCGGTCGCGCTTCCGTTCTCTACCCCAC

        2260      2270      2280      2290      2300      2310      2320      2330      2340
GAGATTGGAACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCACT
CTCTAACCTTGGGGCGAAGTCTAGACCCGAGCCGATGAATGGACGACACGTCGGTACCCAGTTCAACGAACTGGAGAGACACGGAGGTGA
   2350      2360
CCCTTAGCTATAAAATGAGCTTACTT
GGGAATCGATATTTTACTCGAATGAA
```
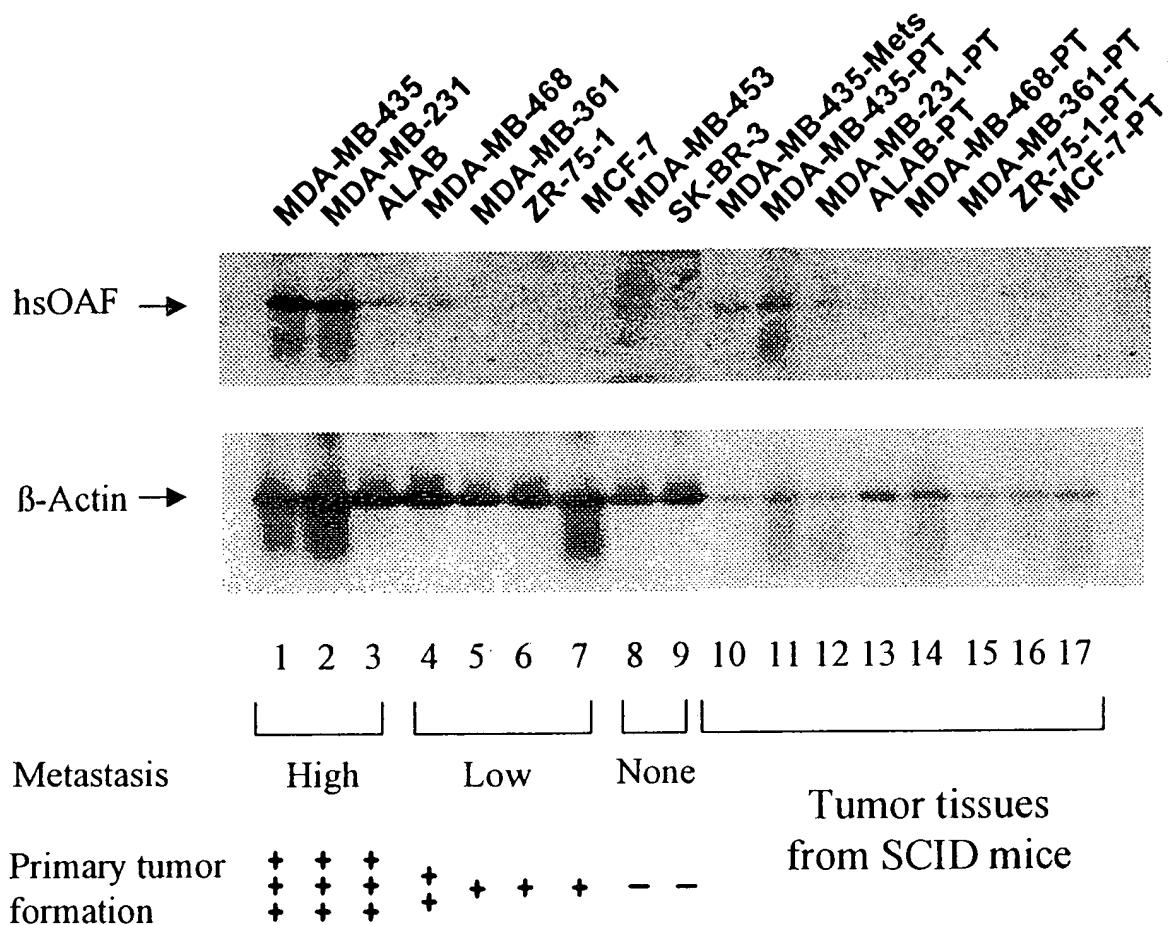
FIGURE 5

FIGURE 6
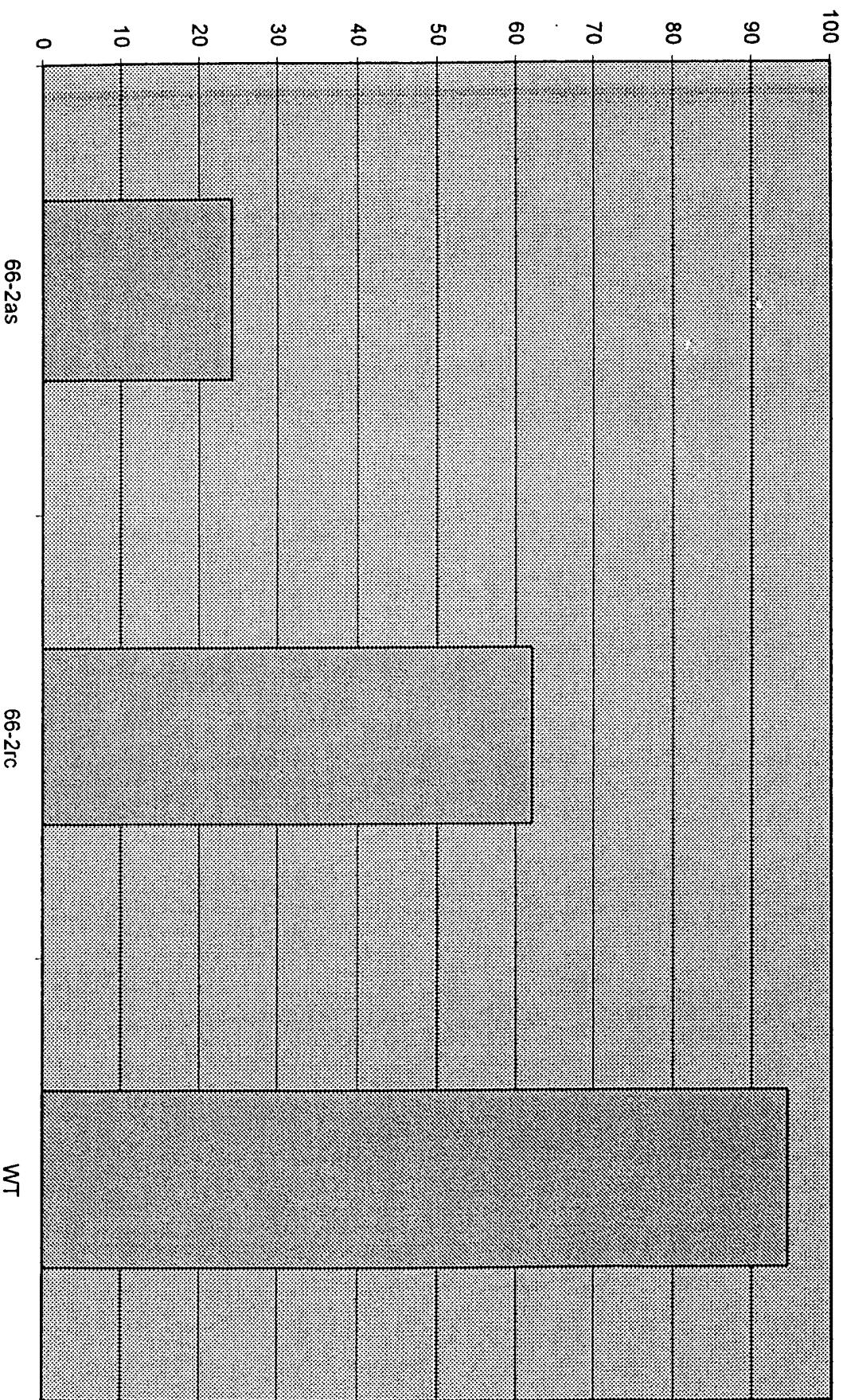
MDA-MB-435 soft agar colonies normalized to WST1

FIGURE 7

hsOAF 1   M R L P G - - - - - - - - - - - - - - - V P L A R 10
OAF   1   M I L K E E H P H Q S I E T A A N A A R Q A Q V R W R M A H L K A L S R T R T R A H G N C C G R V V S K N H F F K H S R 60

hsOAF 11 P A R L L R R P L R A P L L G T G R P A E R R V R V R L P D G Q V T E S V L Q A D S D A H S S S E L R K P D R I V S 70
OAF   61 A F R W F L R C N R V M N A D A F R H S Q R L N R Q N Q G G E V I Q S S T S N I G E R L R T L R F Q K T R R I I T 120

hsOAF 71 F T A R R K K D R K V F R A L I L G S L R K G Q S Q F Q A L R V T Q L Q H N E I R P S E A M A K L R Q K R R A V R Q 130
OAF   121 Q V I D R R N E V Q I L K A L V L G R E E R G Q S Q Y R V M G R A L K F N K G D F L S R A A M A K L R Q K R P H T I R T 180

hsOAF 131 A R R V R G L R H L H M D V A R N F S Q G A L L S P R R L H N V G A R A V D A I R T R Q E D V R F M L R Q - R V D S R V F 189
OAF   181 P R R D K G R R T F T M S S W R Q L N R S L P R T R H R Q G L G A R A M D A T R V R D V D L K A R A R L P R S S I R S L 240

hsOAF 190 R R L P K A S E Q A E L P R R R Q R G D R G K R G V R H Y G L S L A W R R G M R R R G H S R - - - - - R - - - - - - - - - - 236
OAF   241 R A A T E K F P D T L S T R G N E R S S L W A R G L G N L E T G I G W R R G G L R R G K G K G V A G A R S S G A Q Q Q A 300

hsOAF 237 R R R P R R G G R S G Q R S Y S R D F R R R P G R D L G R R D R D P Y P G 273
OAF   301 Q R R N R R G G R K T G R R G T Q R T R R R R G R Q Q G R R D R 332

FIGURE 8A

COS-7   MCF-7

148 KDa——

60 KDa——

42 KDa——

30 KDa——

} hsOAF

- +   - +

FIGURE 8B

MDA-MB-435
MDA-MB-231
ALAB
MDA-MB-468
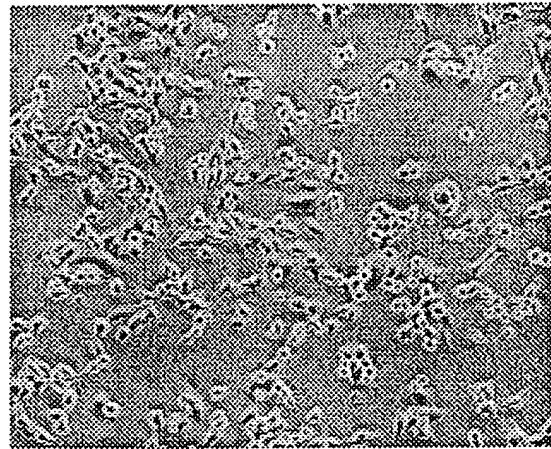MDA-MB-361
ZR-75-1
MCF-7
MDA-MB-453
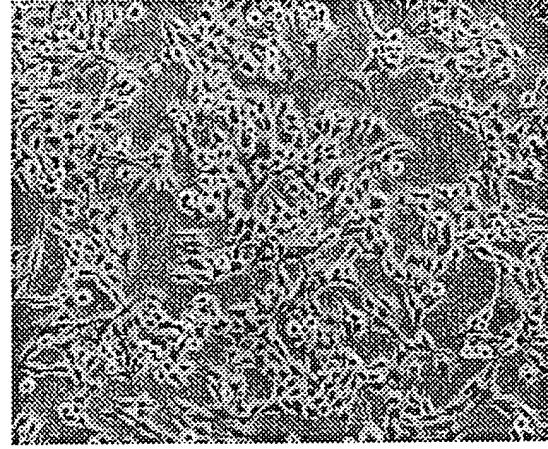SK-BR-3

60 KDa——

42 KDa——
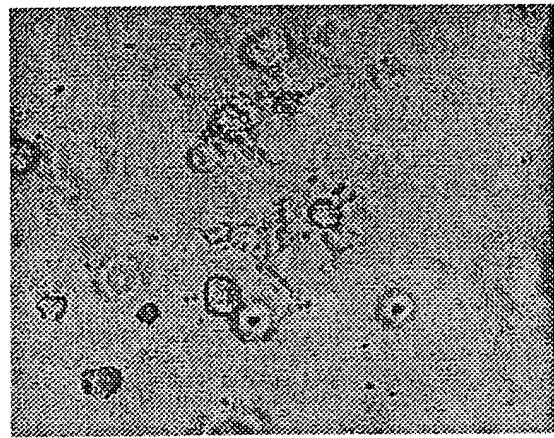
30 KDa——

} hsOAF

FIGURE 9
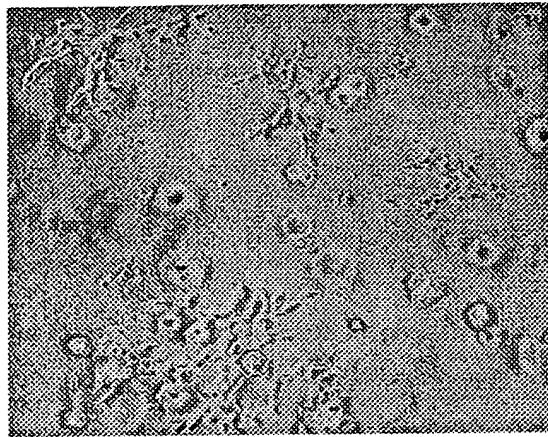
FIGURE 10A
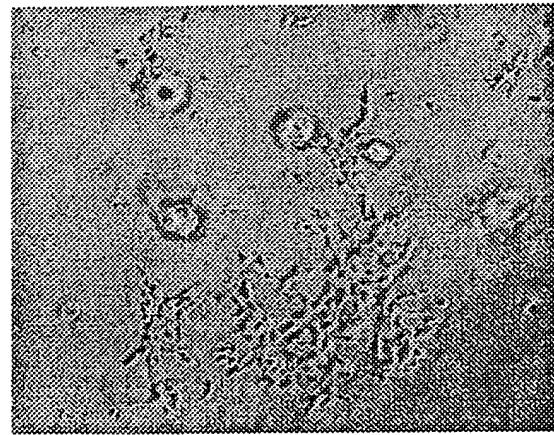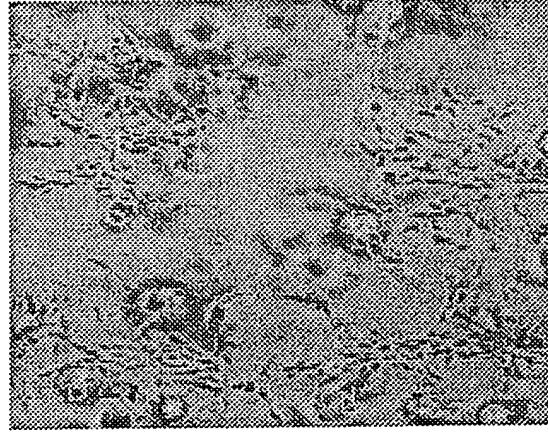
AS

RC

AS+M

Normal

FIGURE 10B

AS

RC

AS+M

Normal

FIGURE 11

```
   1    CCGCGAGGTGCGCGGTCTCTTTAAGGCGGGTCCTGGTGGTTTCTGTTTCCTGAAGGAAGTGACGGGGGGTGGGATTGAATGAAAAGTG
  89    CAAAACACAGGCTCGCAGCGCTGGAGCCCGGGGCCGCGGAGCCGGGCCGGGGCAGCGCCGTCTCCGCCTCGGGGCCGCCGGGGGCGCCCT
 179    GCTGAGCGCTACCCACGTGCGTCCGCGCCACCTCGCGGGCGACCCCGCGGCCAAGGCCCCCGGCGGAGCGGCTCCCGGGCGCCCCGAACT
 269    AGCCCCCAACTTTGGGCGAAGTTTGCCTGCGCCTCTCCCCGCCCCCACGCGGCGCGCCGGGGCCGCGGACGGCAGCGGCCCCCGGGGATG
   1                                                                                         M
 359    CGCCTTCCCGGGGTACCCCTGGCGCGCCCTGCGCTGCTGCTGCTGCTGCCGCTGCTCGCGCCGCTGCTGGGAACGGGTGCGCCGGCCGAG
   2    R  L  P  G  V  P  L  A  R  P  A  L  L  L  L  L  L  P  L  L  A  P  L  L  G  T  G  A  P  A  E
 449    CTGCGGGTCCGCGTGCGGCTGCCGGACGGCCAGGTGACCGAGGAGAGCCTGCAGGCGGACAGCGACGCGGACAGCATCAGCCTCGAGCTG
  32    L  R  V  R  V  R  L  P  D  G  Q  V  T  E  E  S  L  Q  A  D  S  D  A  D  S  I  S  L  E  L
 539    CGCAAGCCCGACGGCACCCTCGTCTCCTTCACCGCCGACTTCAAGAAGGATGTGAAGGTCTTCCGGGCCCTGATCCTGGGGGAGCTGGAG
  62    R  K  P  D  G  T  L  V  S  F  T  A  D  F  K  K  D  V  K  V  F  R  A  L  I  L  G  E  L  E
 629    AAGGGGCAGAGTCAGTTCCAGGCCCTCTGCTTTGTCACCCAGCTGCAGCACAATGAGATCATCCCCAGTGAGGCCATGGCCAAGCTCCGG
  92    K  G  Q  S  Q  F  Q  A  L  C  F  V  T  Q  L  Q  H  N  E  I  I  P  S  E  A  M  A  K  L  R
 719    CAGAAAAATCCCCGGGCAGTGCGGCAGGCGGAGGAGGTTCGGGGTCTGGAGCATCTGCACATGGATGTCGCTGTCAACTTCAGCCAGGGG
 122    Q  K  N  P  R  A  V  R  Q  A  E  E  V  R  G  L  E  H  L  H  M  D  V  A  V  N  F  S  Q  G
 809    GCCCTGCTGAGCCCCCATCTCCACAACGTGTGTGCCGAGGCCGTGGATGCCATCTACACCCGCCAGGAGGATGTCCGGTTCTGGCTGGAG
 152    A  L  L  S  P  H  L  H  N  V  C  A  E  A  V  D  A  I  Y  T  R  Q  E  D  V  R  F  W  L  E
 899    CAAGGTGTGGACAGTTCTGTGTTCGAGGCTCTGCCCAAGGCCTCAGAGCAGGCGGAGCTGCCTCGCTGCAGGCAGGTGGGGGACCGCGGG
 182    Q  G  V  D  S  S  V  F  E  A  L  P  K  A  S  E  Q  A  E  L  P  R  C  R  Q  V  G  D  R  G
 989    AAGCCCTGCGTCTGCCACTATGGCCTGAGCCTGGCCTGGTACCCCTGCATGCTCAAGTACTGCCACAGCCGCGACCGGCCCACGCCCTAC
 212    K  P  C  V  C  H  Y  G  L  S  L  A  W  Y  P  C  M  L  K  Y  C  H  S  R  D  R  P  T  P  Y
1079    AAGTGTGGCATCCGCAGCTGCCAGAAGAGCTACAGCTTCGACTTCTACGTGCCCCAGAGGCAGCTGTGTCTCTGGGATGAGGATCCCTAC
 242    K  C  G  I  R  S  C  Q  K  S  Y  S  F  D  F  Y  V  P  Q  R  Q  L  C  L  W  D  E  D  P  Y
1169    CCAGGCTAGGGTGGGAGCAACCTGGGCGGGTGGCTGCTCTGGGCCCACTGCTCTTCACCAGCCACTAGAGGGGGTGGCAACCCCCACCTG
 272    P  G  *
1259    AGGCCTTATTTCCCTCCCTCCCCACTCCCCTGGCCCTAGAGCCTGGGCCCCTCTGGCCCCATCTCACATGACTGTGAAGGGGGTGTGGCA
1349    TGGCAGGGGGTCTCATGAAGGCACCCCCATTCCCACCCTGTGCCTTCCTTGCGGGCAGAGAGGGAGAGAAGGGCTCCCCAGATCTACACC
1439    CCTCCCTCCTGCATCTCCCCTGGAGTGTTCACTTGCAAGCTGCCAAAACATGATGGCCTCTGGTTGTTCTGTTGAACTCCTTGAACGTTT
1529    AGACCCTAAAAGGAGTCTATACCTGGACACCCACCTCCCCAGCACAACTCCCTTCCCCATGCACACATCTGGAAGGAGCTGGCCCCTCA
1619    GTCCCTTCCTACTCCCCAACAAGGGGCTCACTATCCCCAAAGAAGGAGCTGTTGGGGACCCACGACGCAGCCCCTGTACTGGATTACAGC
1709    ATATTCTCATCTCTGGCCCCGAGGCTGCCTGTGGGGCGAGTGGAGACCTCCCATCACTGAGACAGATCACAGACCACGAGTGCCTTTCCC
1799    GGACCTGGACGTTGCCTCCAAAACAGGCACCAGCTCTTTCCCTCTCTAGACAGAAATATTTTTGTAAGGTTCTGGGGCAGGGAGGGAGCA
1889    TGAAGTACGAGGAAAACTTGAATTCCAGATTTTTAATGCAAAGTATTTATCATTTCTACCAGAAATAAACGTTTTAAGTTTTTACTTGAC
1979    TAATGAGACCCAGAGTTTGGAGAAAACTTTTGGCCAATGCTGCCACCTGATGTCAGAAAGTGTCCCCACACCCTAGCAGTGGCCTATCTT
2069    GGAACAAGAACTTCGAAAGCACCTACTGTGTGCTCAGCCATTTGAGGAAGGAAGGAGGAGAAGGAAGATGTTACTAGGGAAGGATGAGAT
2159    AAAACTTCTGCACCCAAGACAATGAGACAGACATAACTGCAACCGTAGTAAGCCAGTCAGAAATAGCCAGCGCGAAGGCAAGAGATGGGG
2249    TGGAGATTGGAACCCCGCTTCAGATCTGGGCTCGGCTACTTACCTGCTGTGCAGCCATGGGTCAAGTTGCTTGACCTCTCTGTGCCTCCA
2339    CTCCCTTAGCTATAAAATGAGCTTACTT-polyA
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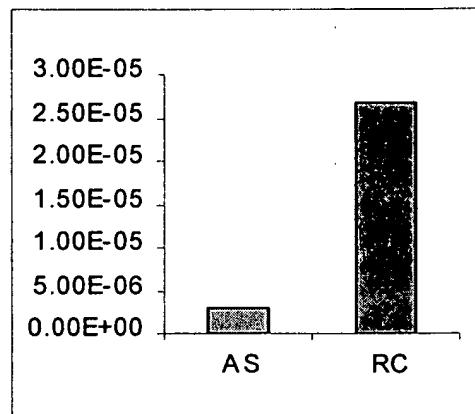
FIGURE 12A

FIGURE 12B